

LONDON  
SCHOOL of  
HYGIENE  
& TROPICAL  
MEDICINE



LSHTM Research Online

Verroken, Alexia; Defourny, Lydwine; le Polain de Waroux, Olivier; Belkhir, Leïla; Laterre, Pierre-François; Delmée, Michel; Glupczynski, Youri; (2016) Correction: Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures. PLOS ONE, 11 (9). e0160537-. ISSN 1932-6203 DOI: <https://doi.org/10.1371/journal.pone.0160537>

Downloaded from: <http://researchonline.lshtm.ac.uk/id/eprint/4656081/>

DOI: <https://doi.org/10.1371/journal.pone.0160537>

#### Usage Guidelines:

Please refer to usage guidelines at <https://researchonline.lshtm.ac.uk/policies.html> or alternatively contact [researchonline@lshtm.ac.uk](mailto:researchonline@lshtm.ac.uk).

Available under license: <http://creativecommons.org/licenses/by/2.5/>

<https://researchonline.lshtm.ac.uk>

CORRECTION

# Correction: Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures

Alexia Verroken, Lydwine Defourny, Olivier le Polain de Waroux, Leïla Belkhir, Pierre-François Laterre, Michel Delmée, Youri Glupczynski

There are numerical errors in the first and penultimate sentences of the second paragraph of the Results under the subheading “Rapid identification and susceptibility test performances.” The correct paragraph is:  $\beta$ LT performed on 164 BSI (P1 and P2 combined) yielded 24 positive, 139 negative and 1 uninterpretable test result due to an incoherent color change of the chromogenic test. All positive  $\beta$ LT results were found in non-natural AmpC EB isolates displaying third generation cephalosporin resistance by complete AST results and subsequently confirmed as ESBL producers. In 7 cases,  $\beta$ LT yielded false-negative results since complete AST and molecular testing identified 6 AmpC producing *Escherichia coli* and 1 VIM metallo-beta-lactamase-producing *P. aeruginosa*, all resistant to third generation cephalosporin. Globally, sensitivity and specificity of  $\beta$ LT were respectively 77.4% and 100%. No erroneous or uninterpretable results were observed with PBP2a testing. Performed on 25 *S. aureus* BSI in P1 and P2, PBP2a was able to detect all 3 MRSA strains (sensitivity and specificity of 100%). Ultimately, 8 BSI (6 in P1 and 2 in P2) were discarded from outcome analysis due to erroneous/uninterpretable rapid test results.

Tables 1 and 2 appear incorrectly in the published article. Please see the correct Tables 1 and 2 and their captions here.



## OPEN ACCESS

**Citation:** Verroken A, Defourny L, le Polain de Waroux O, Belkhir L, Laterre P-F, Delmée M, et al. (2016) Correction: Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures. PLoS ONE 11(9): e0160537. doi:10.1371/journal.pone.0160537

**Published:** September 22, 2016

**Copyright:** © 2016 Verroken et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Table 1. Distribution of microorganisms and main resistances of all bloodstream infections across the three study periods.** 3GC, third generation cephalosporin (cefotaxime, ceftriaxone, ceftazidime); AST, antimicrobial susceptibility testing; BSI, bloodstream infection; carbapenem (imipenem, meropenem); ID, identification; P0, pre-intervention period; P1, intervention period 1; P2, intervention period 2. Natural AmpC producers identified during the study periods: *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Hafnia alvei*, *Serratia marcescens*. Non-natural AmpC producers identified during the study periods: *Citrobacter koseri*, *Escherichia coli*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Proteus vulgaris*, *Salmonella* spp.

Microorganism Resistance	P0	P1			P2		
	n BSI (%)	n BSI (%)	n BSI	n BSI	n BSI (%)	n BSI	n BSI
	final outcome analysis	final outcome analysis	with failed ID	with failed partial AST	final outcome analysis	with failed ID	with failed partial AST
Gram-positive bacteria	50 (37.3)	40 (35.7)	8	0	44 (28.6)	7	0
Staphylococci	25	22	3	0	24	2	0
Staphylococcus aureus	14	11	1	0	14	0	0
methicillin	1	1	0	-	2	-	-
Coagulase negative Staphylococci	11	11	2	0	10	2	0
Enterococci	12	11	1	0	9	1	0
Streptococci	9	7	2	0	10	4	0
Other Gram-positive bacteria	4	0	2	0	1	0	0
Gram-negative bacteria	77 (57.5)	71 (63.4)	1	6	107 (69.5)	2	2
Enterobacteriaceae	71	63	0	5	103	1	2
natural AmpC producers	5	6	0	0	11	0	0
3GC	2	1	-	-	4	-	-
carbapenem	0	0	-	-	0	-	-
non-natural AmpC producers	66	57	0	5	92	1	2
3GC	10	6	-	5	18	0	2
carbapenem	0	0	-	0	0	0	0
Non fermenters	6	6	1	1	4	1	0
Pseudomonas aeruginosa	3	4	0	1	3	1	0
3GC	0	0	-	1	0	0	-
carbapenem	0	0	-	1	0	0	-
Other non fermenters	3	2	1	0	1	0	0
Other Gram-negative bacteria	0	2	-	0	0	0	0
Anaerobes	6 (4.5)	0 (0.0)	6	0	2 (1.3)	6	0
Yeast	1 (0.7)	1 (0.9)	2	0	1 (0.6)	3	0
TOTAL	134 (100)	112 (100)	17	6	154 (100)	18	2

doi:10.1371/journal.pone.0160537.t001

**Table 2. Time to identification and time to partial/complete susceptibility results of all bloodstream infections during pre-intervention and intervention period 1 and 2.**

Time to identification			
Phase	Method	BSI (n)	Mean time to ID (hours)
<b>P0</b>	<b>TOTAL</b>	<b>134</b>	<b>28.3</b>
	Subculture MALDI-TOF MS	134	28.3
	Early MALDI-TOF MS	-	-
	Direct MALDI-TOF MS	-	-
<b>P1</b>	<b>TOTAL</b>	<b>112</b>	<b>10.2</b>
	Subculture MALDI-TOF MS	23	15.9
	Early MALDI-TOF MS	65	10.6
	Direct MALDI-TOF MS	24	3.6
<b>P2</b>	<b>TOTAL</b>	<b>154</b>	<b>10.8</b>
	Subculture MALDI-TOF MS	32	17.1
	Early MALDI-TOF MS	96	10.7
	Direct MALDI-TOF MS	26	4.0
Time to complete susceptibility result			
Phase	Method	BSI (n)	Mean time to complete AST result (hours)
<b>P0</b>	<b>TOTAL</b>	<b>134</b>	<b>44.7</b>
	Phoenix from subculture	58	46.9
	Phoenix from young subculture	-	-
	Direct Phoenix	48	28.3
	Manual testing from subculture	28	68.3
	Manual testing from young subculture	-	-
<b>P1</b>	<b>TOTAL</b>	<b>112</b>	<b>32.4</b>
	Phoenix from subculture	28	41.2
	Phoenix from young subculture	23	32.2
	Direct Phoenix	45	25.6
	Manual testing from subculture	7	49.1
	Manual testing from young subculture	9	27.3
<b>P2</b>	<b>TOTAL</b>	<b>154</b>	<b>32.6</b>
	Phoenix from subculture	34	41.6
	Phoenix from young subculture	81	29.9
	Direct Phoenix	22	22.2
	Manual testing from subculture	8	52.2
	Manual testing from young subculture	9	30.9
Time to partial susceptibility result			
Phase	Method	BSI (n)	Mean time to partial susceptibility testing result (hours)
<b>P1</b>	<b>TOTAL</b>	<b>72</b>	<b>11.8</b>
	Culture $\beta$ LT	20	17.9
	Young subculture $\beta$ LT	29	11.2
	Direct $\beta$ LT	12	3.7
	Culture PBP2a	3	15.3
	Young subculture PBP2a	6	12
	Direct PBP2a	2	2

(Continued)

**Table 2.** (Continued)

P2	TOTAL	109	11.7
	Culture $\beta$ LT	29	16.8
	Young subculture $\beta$ LT	51	11.1
	Direct $\beta$ LT	15	3.6
	Culture PBP2a	4	20.2
	Young subculture PBP2a	9	8.8
	Direct PBP2a	1	6

doi:10.1371/journal.pone.0160537.t002

## Reference

1. Verroken A, Defourny L, le Polain de Waroux O, Belkhir L, Laterre P-F, Delmée M, et al. (2016) Clinical Impact of MALDI-TOF MS Identification and Rapid Susceptibility Testing on Adequate Antimicrobial Treatment in Sepsis with Positive Blood Cultures. PLoS ONE 11(5): e0156299. doi: [10.1371/journal.pone.0156299](https://doi.org/10.1371/journal.pone.0156299) PMID: [27228001](https://pubmed.ncbi.nlm.nih.gov/27228001/)